```
   1  TCGAACTCAC  TCACCTCCCC  TCTCACCTCA  CTGCCCTCAC  CAGCCAGCCT
  51  CTTGTCAAGT  GATCAGGCTG  TCAACCAACT  TCTCTAGGAT  AAGGTTTCAG
 101  GTCAGCCTGT  GTGTATAAGA  CCAGTGCCAA  GCCAGAAGCA  GCAGAGACAA
 151  CAGTGAATGA  CAAGGAGGGG  CCATCCAATC  CCTGCTGCCA  CCTCCTGGGA
 201  TGGAGCCCTA  GGGAGCCCCT  GTGCTGCCCC  TGCCGTGGCA  GGACTCACAG
 251  CCCCACCGCT  GCACTGAAGC  CCAGGGCTGT  GGAGCAGCTC  TCTCCTTGGA
 301  CTCCTCTCGG  CCCTAAAGGG  ACTGGGCAGA  GCCTTCCAGG  ACTATGGTTG
 351  GACTGAAGCC  TTCAGACGTG  CCTCCCACCA  TGGCTGTGAA  GTTCCTGGGG
 401  GCAGGCACAG  CAGCCTGTTT  TGCTGACCTC  GTTACCTTTC  CACTGGACAC
 451  AGCCAAGGTC  CGCCTGCAGA  TCCAGGGGGA  GAACCAGGCG  GTCCAGACGG
 501  CCCGGCTCGT  GCAGTACCGT  GGCGTGCTGG  GCACCATCCT  GACCATGGTG
 551  CGGACTGAGG  GTCCCTGCAG  CCCCTACAAT  GGGCTGGTGG  CCGGCCTGCA
 601  GCGCCAGATG  AGCTTCGCCT  CCATCCGCAT  CGGCCTTTAC  GACTCCGTCA
 651  AGCAGGTGTA  CACCCCCAAA  GGCGCGGACA  ACTCCAGCCT  CACTACCCGG
 701  ATTTTGGCCG  GCTGCACCAC  AGGAGCCATG  GCGGTGACCT  GTGCCCAGCC
 751  CACAGATGTG  GTGAAGGTCC  GATTTCAGGC  CAGCATACAC  CTCGGGCCAT
 801  CCAGGAGCGA  CAGAAAATAC  AGCGGGACTA  TGGACGCCTA  CAGAACCATC
 851  GCCAGGGAGG  AAGGAGTCAG  GGGCCTGTGG  AAAGGAACTT  TGCCCAACAT
 901  CATGAGGAAT  GCTATCGTCA  ACTGTGCTGA  GGTGGTGACC  TACGACATCC
 951  TCAAGGAGAA  GCTGCTGGAC  TATCACCTGC  TCACTGACAA  CTTCCCCTGC
1001  CACTTTGTCT  CTGCCTTTGG  AGCCGGCTTC  TGTGCCACAG  TGGTGGCCTC
1051  CCCGGTGGAC  GTGGTGAAGA  CCCGGTATAT  GAACTCACCT  CCAGGCCAGT
1101  ACTTCAGCCC  CCTCGACTGT  ATGATAAAGA  TGGTGGCCCA  GGAGGGCCCC
1151  ACAGCCTTCT  ACAAGGGATT  TACACCCTCC  TTTTTGCGTT  TGGGATCCTG
1201  GAACGTGGTG  ATGTTCGTAA  CCTATGAGCA  GCTGAAACGG  GCCCTGATGA
1251  AAGTCCAGAT  GTTACGGGAA  TCACCGTTTT  GAACAAGACA  AGAAGGCCAC
1301  TGGTAGCTAA  CGTGTCCGAA  ACCAGTTAAG  AATGGAAGAA  AACGGTGCAT
```

FIG.1A

```
1351 CCACGCACAC ATGGACACAG ACCCACACAT GTTTACAGAA CTGTTGTTTA

1401 CTTGTTGCTG ATTCAAGAAA CAGAAGTAGA AGAGAGAGGA TTCTGGTCTT

1451 CACTGCCATG CCTCAAGAAC ACCTTTGTTT TGCACTGACA AGATGGAAAA

1501 TAAATTATAT TAATTTTTGA AACCCATTAG GCATGCCTAA TATTTAGGCA

1551 AGAGAAAATA AACCAAGATA GATCCATTTG GACAAAATGG AAGGTTGGAG

1601 ACGTGTATCC CCGTGAAATC TGGTCAGATA ATGAATGATA AGCAGGAAGG

1651 ATGGCAAGCA CGGGACAGGA GGGGCCCACA ATGGAGTGGG AGATCAGCCA

1701 CGGAGCCTGG AGGGACGCCA CCCAGCAACA CAGAGCTGGC GACTGCAGCT

1751 GCACCATCAC ACATGCATCA TCAGCCTATT TGTAATATGT CTGCCACAGA

1801 GAGTCCTTTG GGATTCTAGG AAACCCAAGG AACAAGAGAA AAAACTAGAG

1851 CCTGTGCTAA AGAAGCCTGC TGGGCCCATG TGAGGCTGGG GTCGTAAATA

1901 TTCCCCGACG ACACTGAAGA ATCAAGAGGG CAGCCCCCAC TTCTCCTACA

1951 AAATGGAGGG AGCCATCCCT TCCCTGTCCA CCTCACCAGG GGTGCTATGA

2001 CATGCAAGTG AGAAGCTGGG CATGAACGCA CTTTATAAAA GCAAAAGCTC

2051 TGTGTAAATC TAACTACAAG GACAATGCCT TGGGAGAGAT TTTGTCGGGA

2101 CAGAGAGGAG TTGCCAGGGA AGAAGGTTTG AAAGATACGG TTGTCTAGAG

2151 GTGAGACCAA AGGATCCAGA GACTTGGGGA CCAGAGGTGA CAGTGGATGA

2201 CGTGAAGCCA CAGGAGCCCC ACCCCCATGC AGCTTTTTCC CCACCCCCCC

2251 CACCACGCGC TCAATCATGA GTACCTCAAA GGATTGTTGG CTTGGGGGA

2301 AAAGAGGTGG ATTCCTGGGC AAGAACCTAA AGTAGCAGGA  (SEQ ID NO.11)
```

FIG.1B

```
1    TCGAACTCACTCACTCCCCTCTCACCTCACTGCCCTCACCAGCGCCAGCCTCTTGTCAAGT    60
     -----+---------+---------+---------+---------+---------+
     AGCTTGAGTGAGTGGAGGGGAGAGTGGAGTGACGGGAGTGGTCGGCGGTCGGAGAACAGTTCA

61   GATCAGGCTGTCAACCAACTTCTCTAGGATAAGGTTTCAGGTCAGCCTGTGTGTATAAGA    120
     -----+---------+---------+---------+---------+---------+
     CTAGTCCGACAGTTGGTTGAAGAGATCCTATTCCAAAGTCCAGTCGGACACACATATTCT

121  CCAGTGCCAAGCCAGGAAGCAGCAGAGACAACAGTGAATGACAAGGAGGGGCCATCCAATC    180
     -----+---------+---------+---------+---------+---------+
     GGTCACGGTTCGGTCTTCGTCGTCTCTGTTGTCACTTACTGTTCCTCCCGGTACCTTAG

181  CCTGCTGCCACCTCCTGGGATGGAGCCCTAGGAGGAGCCCCTGTGCTGCCCCTGCCGTGGCA    240
     -----+---------+---------+---------+---------+---------+
     GGACGACGGTGGAGGACCCTACCTCGGGATCCCTCGGGGACACGACGGGGACGGCACCGT

241  GGACTCACAGCCCCACCGCTGCACTGAAGCCCAGGGCTGTGTGGAGCAGCTCTCTCCTTGGA    300
     -----+---------+---------+---------+---------+---------+
     CCTGAGTGTCGGGGTGGCGACGTGACTTCGGGTCCCGACACCTCGTCGAGAGGAACCT

301  CTCCTCTCTCGGGCCCTAAAGGGACTGGGCAGAGCCTTCCAGGACTATGGTTGGACTGAAGCC    360
     -----+---------+---------+---------+---------+---------+
     GAGGAGAGAGCCGGGATTTCCCTGACCGTCTCGGAAGGTCCTGATACCAACCTGACTTCGG
                                                    M  V  G  L  K  P

361  TTCAGAGCGTGCCTCCCACCATGGCTGTGTGAAGTTCCTGGGGGGCACAGCAGCCTGTTT    420
     -----+---------+---------+---------+---------+---------+
     AAGTCTGCACGGAGGGTGGTACCGACACTTCAAGGACCCCGTCGTCGTCGGACAAA
      S  D  V  P  P  T  M  A  V  K  F  L  G  A  G  T  A  A  C  F
```

FIG.2A

```
421
     TGCTGACCTCGTTACCTTTCCACTGGACACAGCCAAGGTCCGCCTGCAGATCCAGGGGGA
     --------+---------+---------+---------+---------+---------+   480
     ACGACTGGAGCAATGGAAAGGTGACCTGTGTCGGTTCCAGGCGGCGACGTCTAGGTCCCCT
     A  D  L  V  T  F  P  L  D  T  A  K  V  R  L  Q  I  Q  G  E

461
     GAACCAGGGCGGTCCAGACGGCCCGGCTCGTGCAGTACCGTGGCGTGCTGGGCACCATCCT
     --------+---------+---------+---------+---------+---------+   540
     CTTGGTCCGCCAGGTCTGCCGGGCCGAGCACGTCATGGCACCGCACCGTGGTAGGA
     N  Q  A  V  Q  T  A  R  L  V  Q  Y  R  G  V  L  G  T  I  L

541
     GACCATGGTGCGGACTGAGGGTCCCTGCAGCCCTACAATGGGCTGGTGGCCGGGCTGCA
     --------+---------+---------+---------+---------+---------+   600
     CTGGTACCACGCCTGACTCCCAGGACGTCGGGGATGTTACCGACCACCGGCCGGACGT
     T  M  V  R  T  E  G  P  C  S  P  Y  N  G  L  V  A  G  L  Q

601
     GCGGCCAGATGAGCTTCGCCTCCATCAGCATCGGCCTTTACGACTCCGTCAAGCAGGTGTA
     --------+---------+---------+---------+---------+---------+   660
     CGCGGTCTACTCGAAGCGGAGGTAGTCGTAGCCGGAAATGCTGAGGCAGTTCGTCCACAT
     R  Q  M  S  F  A  S  I  R  I  G  L  Y  D  S  V  K  Q  V  Y

661
     CACCCCCAAAGGCGGCGGACAACTCCAGCCTCACTACCCGGATTTTGGCCGGCTGCACCAC
     --------+---------+---------+---------+---------+---------+   720
     GTGGGGGGTTTCCGCGCCTGTTGAGGTCGGAGTGATGGGCCTAAAACCGGCCGACGTGGTG
     T  P  K  G  A  D  N  S  S  L  T  T  R  I  L  A  G  C  T  T
```

FIG.2B

```
721  AGGAGCCATGGGCGGTGACCTGTGCCCAGCCCACAGATGTGGTGAAGGTCCGATTTCAGGC
     ----------+---------+---------+---------+---------+---------+  780
     TCCTCGGTACCGCCACTGGACACGGGTCGGGTGTCTACACCACTTCCAGGCTAAAGTCCG
      G  A  M  A  V  T  C  A  Q  P  T  D  V  V  K  V  R  F  Q  A

781  CAGCATACACCTCGGGCCATCCAGGAGCGACAGAAAATACAGCGGGACTATGGACGCCTA
     ----------+---------+---------+---------+---------+---------+  840
     GTCGTATGTGGAGCCCGGTAGGTCCTCGCTGTCTTTTATGTCGCCCTGATACCTGCGGAT
      S  I  H  L  G  P  S  R  S  D  R  K  Y  S  G  T  M  D  A  Y

841  CAGAACCATCGCCCAGGGAGGAAGGAGTCAGGGGCCTGTGGAAAGGAACTTTGCCCAACAT
     ----------+---------+---------+---------+---------+---------+  900
     GTCTTGGTAGCGGGTCCCTCCTTCCTCAGTCCCGGACACTTTCCTTGAAACGGGTTGTA
      R  T  I  A  R  E  E  G  V  R  G  L  W  K  G  T  L  P  N  I

901  CATGAGGAATGCTATGTCAACTGTGCTGAGGTGGTGACCTACGACATCCTCAAGGAGAA
     ----------+---------+---------+---------+---------+---------+  960
     GTACTCCTTACGATAGCAGTTGACACGACTCCACCACTGGATGCTGTAGGAGTTCCTCTT
      M  R  N  A  I  V  N  C  A  E  V  V  T  Y  D  I  L  K  E  K

961  GCTGCTGGACTATCACCTGCTCACTGACAACTTCCCCTGCCACTTTGTCTCTGCCTTTGG
     ----------+---------+---------+---------+---------+---------+  1020
     CGACGACCTGATAGTGGACGAGTGACTGTTGAAGGGGACGGTGAAACAGAGACGGAAACC
      L  L  D  Y  H  L  L  T  D  N  F  P  C  H  F  V  S  A  F  G

1021 AGCCGGCTTCTGTGCCACAGTGGTGGCCTCCCCGGTGGACGTGGTGAAGACCCGGTATAT
     ----------+---------+---------+---------+---------+---------+  1080
     TCGGCCGAAGACACGGTGTCACCACCGGAGGGGCCACCTGCACCACTTCTGGGCCATATA
      A  G  F  C  A  T  V  V  A  S  P  V  D  V  V  K  T  R  Y  M
```

FIG.2C

GAACTCACCTCCAGGCCAGTACTTCAGCCCCCTCGACTGTGTATGATAAAGATGGTGGCCCA
1081 ----+----+----+----+----+----+ 1140
CTTGAGTGGAGGTCCGGTCATGAACTCGGGGGAGCTGACATACTATTTCTACCACCGGGT
N S P P G Q Y F S P L D C M I K M V A Q

GGAGGGGCCCCACAGCCTTCTACAAGGGATTTACACCCTCCTTTTGCGTTTGGGATCCTG
1141 ----+----+----+----+----+----+ 1200
CCTCCCGGGGTGTCGGAAGATGTTCCCTAAATGTGGGAGGAAAAACGCAAACCCTAGGAC
E G P T A F Y K G F T P S F L R L G S W

GAACGTGGTGATGTTCGTAACCTATGAGCAGCTGAAACGGGCCCTGATGAAAGTCCAGAT
1201 ----+----+----+----+----+----+ 1260
CTTGCACCACTACAAGCATTGGATACTCGTCGCCCGGGACTACTTTCAGGTCTA
N V M F V T Y E Q L K R A L M K V Q M

GTTACGGGGAATCACCGTTTTGAACAAGACAAGAGAGGCCACTGGTAGCTAACGTGTCCGAA
1261 ----+----+----+----+----+----+ 1320
CAATGCCCTTAGTGGCAAAACTTGTTCTGTTCTTCCGGTGACCATCGATTGCACAGGCTT
L R E S P F * (SEQ ID NO.12)

ACCAGTTAAGAATGGAAGAAGAAAACGGTGCATCCACGCACACATGGACACAGACCCACACAT
1321 ----+----+----+----+----+----+ 1380
TGGTCAATTCTTACCTTCTTTTGCCACGTAGGTGGTGTACCTGTGTCTGGGTGTGTA

FIG.2D

```
1381  GTTTACAGAACTGTTGTTGTTACTTGTTGCTGATTCAAGAAACAGAAGTAGAAGAGAGAGGA
      ----------+---------+---------+---------+---------+---------+ 1440
      CAAATGTCTTGACAACAAATGAACAACGACTAAGTTCTTGTCTTCATCTTCTCTCTCCT

1441  TTCTGGTCTTCACTGCCATGCCTCAAGAACACCTTTGTTTGCACTGACAAGATGGAAAA
      ----------+---------+---------+---------+---------+---------+ 1500
      AAGACCAGAAGTGACGGTACGGGAGTTCTTGTGGAAACAAAACGTGACTGTTCTACCTTTT

1501  TAAATTATATATTAATTTTTGAAACCCATTAGGCATGCCTAATATATTAGGCAAGAGAAAATA
      ----------+---------+---------+---------+---------+---------+ 1560
      ATTTAATATAATTAAAAACTTTGGGTAATCCGTACGGATTATAAATCGTTCTTTTTAT

1561  AACCAAGATAGATCCATTTGGACAAAATGGAAGGTTGGAGACGTGTATCCCGTGAAATC
      ----------+---------+---------+---------+---------+---------+ 1620
      TTGGTTCTATCTAGGTAAACCTGTTTTACCTTCCAACCTCTGCACATAGGGGCACTTTAG

1621  TGGTCAGATAATGATAAGCAGGAAGGATGGCAAGCACGGGACAGGAGGGGCCCACA
      ----------+---------+---------+---------+---------+---------+ 1680
      ACCAGTCTATTACTTACTATTCGTCCTTCCTACGTTCGGTGCCCTGTCCTCCCGGGTGT

1681  ATGGAGTGGGAGATCAGCCACGGAGCCTGGAGGGACGCCACCCAGCAACACAGAGCTGGC
      ----------+---------+---------+---------+---------+---------+ 1740
      TACCTCACCCTCTAGTCGGTGCCTCGGACCTCCCTGCGGTGGGTCGTTGTGTCTCGACCG

1741  GACTGCAGCTGCACCATCACACATGCATCATCAGCCTATTTGTAATATGTCTGCCACAGA
      ----------+---------+---------+---------+---------+---------+ 1800
      CTGACGTCGACGTGGTAGTGTGTAGTAGTCGGATAAACATTATACAGACGGTGTCT

1801  GAGTCCCTTTGGGATTCTAGGAAACCCAAGGAACAAGAGAGAAAAAACTAGAGCCTGTGCTAA
      ----------+---------+---------+---------+---------+---------+ 1860
      CTCAGGAAACCCTAAGATCCTTTGGGTTCCTTGTTCTCTTTTTGATCTCGGACACGATT
```

FIG.2E

1861 AGAAGCCTGCTGGGCCCATGTGTGAGGCTGGGGTCGTAAATATTCCCGACGACACTGAAGA
     ----+----+----+----+----+----+----+----+----+----+----+----+ 1920
     TCTTCGGACGACCCGGGTACACTCCGACCCCAGCATTTATAAGGGCTGCTGTGACTTCT

1921 ATCAAGAGGGCAGCCCCACTTCTCCTACAAAATGGAGGGAGCCATCCCTTCCCTGTCCA
     ----+----+----+----+----+----+----+----+----+----+----+----+ 1980
     TAGTTCTCCCGTCGGGGGTGAAGAGGATGTTTACCTCCCTCGGTAGGGAAGGGACAGGT

1981 CCTCACCAGGGGTGCTATGACATGCAAGTGAGAAGCTGGGCATGAACGCACTTTATAAAA
     ----+----+----+----+----+----+----+----+----+----+----+----+ 2040
     GGAGTGGTCCCCACGATACTGTACGTTCACTCTTCGACCCGTACTTGCGTGAAATATTTT

2041 GCAAAAGCTCTGTGTAAATCTAACTACACAAGGACAAATGCCTTGGGAGAGATTTTGTCGGGA
     ----+----+----+----+----+----+----+----+----+----+----+----+ 2100
     CGTTTTCGAGACACATTTAGATTGATGTTCCTGTTACGGAACCCTCTCTAAAACAGCCCT

2101 CAGAGAGGGAGTTGCCAGGGGAAGAAAGGTTTGAAAGATACGGTTGTCTAGAGGTGAGACCAA
     ----+----+----+----+----+----+----+----+----+----+----+----+ 2160
     GTCTCTCCTCAACGGTCCCCTTCTTCCAAACTTTCTATGCCAACAGATCTCCACTCTGGTT

2161 AGGATCCAGAGACTTGGGGACCAGAGGTGACAGTGGATGACGTGAAGCCACAGGAGCCCC
     ----+----+----+----+----+----+----+----+----+----+----+----+ 2220
     TCCTAGGTCTCTGAACCCCTGGTCTCCACTGTCACCTACTGCACTTCGGTGTCCTCGGGG

2221 ACCCCCATGCAGCTTTTTCCCCACCCCCCACCACGCGCTCAATCATGAGTACCTCAAA
     ----+----+----+----+----+----+----+----+----+----+----+----+ 2280
     TGGGGGTACGTCGAAAAAGGGGTGGGGGGGTGGTGCGCGAGTTAGTACTCATGGAGTTT

2281 GGATTGTTTGGGCTTGGGGGGAAAAGAGGTGGATTCCTGGGCAAGAACCTAAAGTAGCAGGA
     ----+----+----+----+----+----+----+----+----+----+----+----+ 2340
     CCTAACAACCCGAACCCCCTTTTCTCCACCTAAGGACCCGTTCTTTGGATTTCATCGTCCT

FIG.2F

```
  1 MVGLKPSSDP PTMAVKFLGA GTAACFADLV TFPLDTAKVR LQIQGENQAV

 51 QTARLVQYRG VLGTILTMVR TEGPCSPYNG LVAGLQRQMS FASIRIGLYD

101 SVKQVYTPKG ADNSSLTTRI LAGCTTGAMA VTCAQPTDVV KVRFQASIHL

151 GPSRSDRKYS GTMDAYRTIA REEGVRGLWK GTLPNIMRNA IVNCAEVVTY

201 DILKEKLLDY HLLTDNFPCH FVSAFGAGFC ATVVASPVDV VKTRYMNSPP

251 GQYFSPLDCM IKMVAQEGPT AFYKGFTPSF LRLGSWNVVM FVTYEQLKRA

301 LMKVQMLRES PF* (SEQ ID NO.12)
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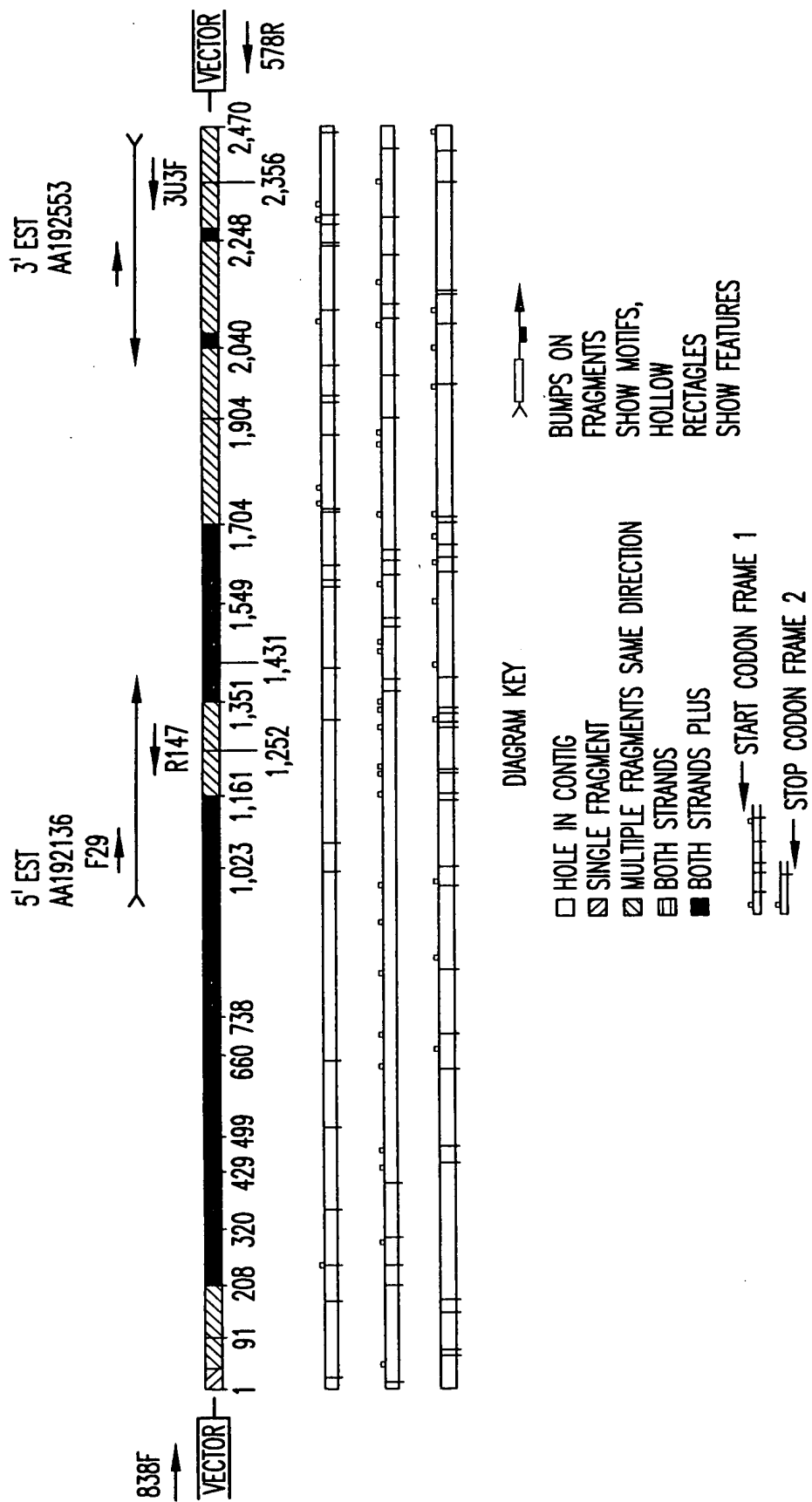
FIG.3

UCP3
(13 hr. exp.)

FIG.4A

Pancreas
Kidney
Skeletal Muscle
Liver
Lung
Placenta
Brain
Heart

MW(kb)
9.5
7.5
4.4
2.4
1.4

UCP3
(0.5 hr exp)

FIG.4B

Pancreas
Kidney
Skeletal Muscle
Liver
Lung
Placenta
Brain
Heart

MW(kb)
9.5
7.5
4.4
2.4
1.4

UCP3 and β-actin
(0.5 hr. exp.)

FIG.4C

Pancreas
Kidney
Skeletal Muscle
Liver
Lung
Placenta
Brain
Heart

MW(kb)
9.5
7.5
4.4
2.4
1.4
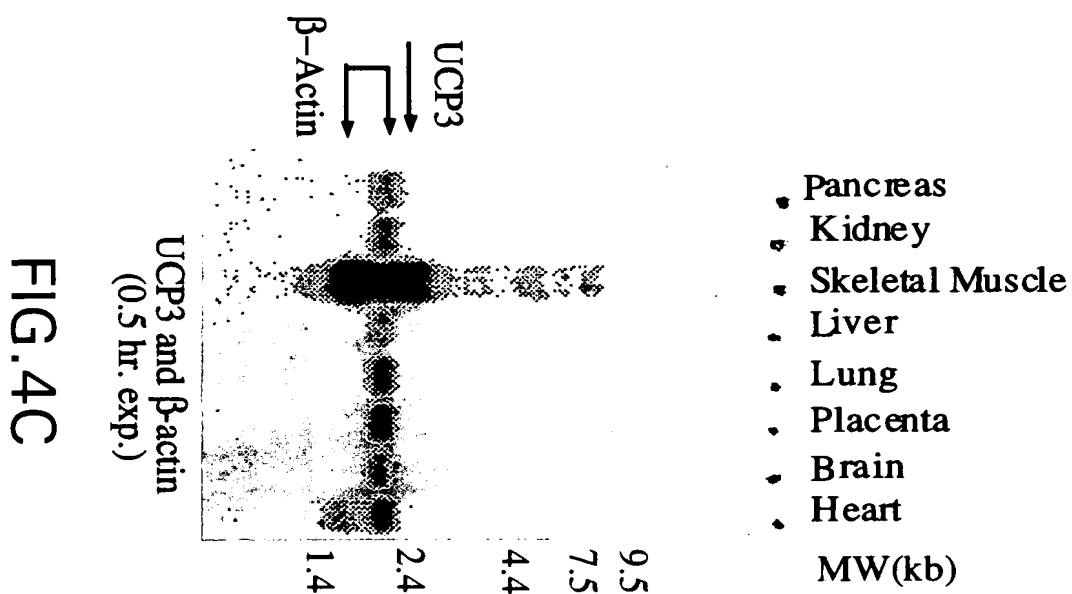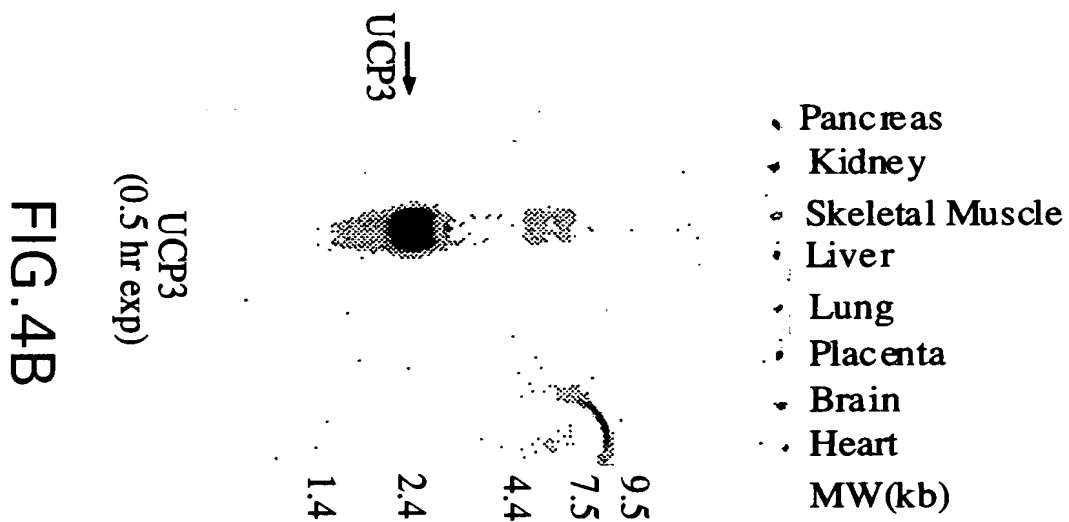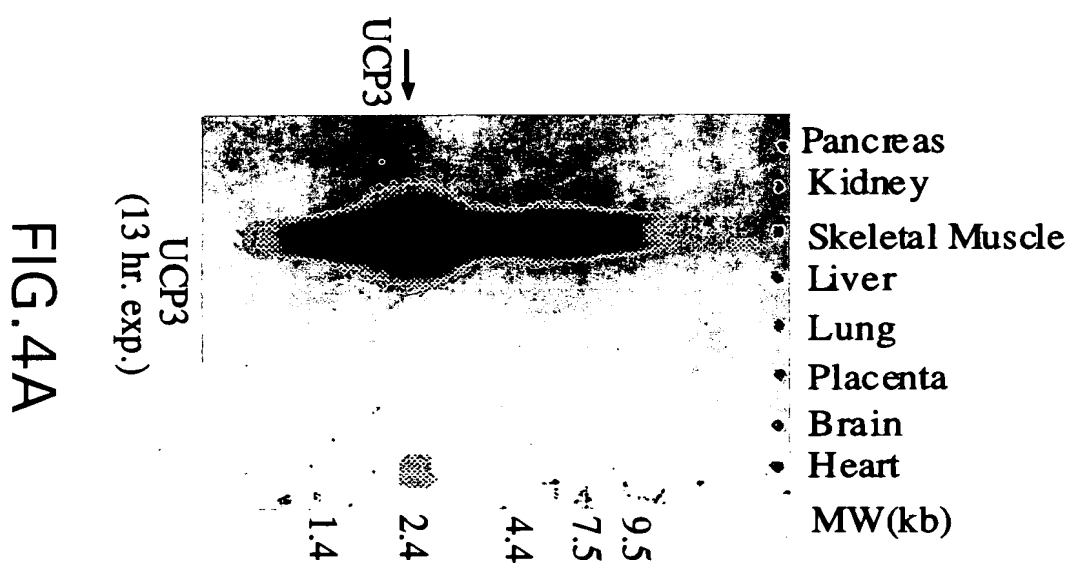
FIG.5

```
  1 CCAGGAACAG CAGAGACAAC AGTGAATGGT GAGGCCCGGC CGTCAGATCC

 51 TGCTGCTACC TAATGGAGTG GATCCTTAGG GTCGCCCTGC ACTACCCAAC

101 CTTGGCTAGA CGCACAGCTT CCTCCCTGAA CTGAAGCAAA AGATTGCCAG

151 CCAAGCTCTC TCCTCGGACC TCCATAGGCA GCAAAGGAAC CAGGCCCATT

201 CCCCGGGACC ATGGTTGGAC TTCAGCCCTC CGAAGTGCCT CCCACAACGG

251 TTGTGAAGTT CCTGGGGGCC GGCACTGCGG CCIGTTTTGC GGACCTCCTC

301 ACTTTTCCCC TGGACACCGC CAAGGTCCGT CTGCAGATCC AAGGGGAGAA

351 CCCAGGGGCT CAGAGCGTGC AGTACCGCGG TGTGCTGGGT ACCATCCTGA

401 CTATGGTGCG CACAGAGGGT CCCCGCAGCC CCTACAGCGG ACTGGTCGCT

451 GGCCTGCACC GCCAGATGAG TTTTGCCTCC ATTCGAATTG GCCTCTACGA

501 CTCTGTCAAG CAGTTCTACA CCCCCAAGGG AGCGGACCAC TCCAGCGTCG

551 CCATCAGGAT TCTGGCAGGC TGCACGACAG GAGCCATGGC AGTGACCTGC

601 GCCCAGCCCA CGGATGTGGT GAAGGTCCGA TTTCAAGCCA TGATACGCCT

651 GGGAACTGGA GGAGAGAGGA AATACAGAGG GACTATGGAT GCCTACAGAA

701 CCATCGCCAG GGAGGAAGGA GTCAGGGGCC TGTGGAAAGG GACTTGGCCC

751 AACATCACAA GAAATGCCAT TGTCAACTGT GCTGAGATGG TGACCTACGA

801 CATCATCAAG GAGAAGTTGC TGGAGTCTCA CCTGTTTACT GACAACTTCC

851 CCTGTCACTT TGTCTCTGCC TTTGGAGCTG GCTTCTGTGC CACAGTGGTG

901 GCCTCCCCGG TGGATGTGGT AAAGACCCGA TACATGAACG CTCCCCTAGG

951 CAGGTACCGC AGCCCTCTGC ACTGTATGCT GAAGATGGTG GCTCAGGAGG
```

FIG.6A

```
1001 GACCCACGGC CTTCTACAAA GGATTTGTGC CCTCCTTTCT GCGTCTGGGA

1051 GCTTGGAACG TGATGATGTT TGTAACATAT GAGCAACTGA AGAGGGCCTT

1101 AATGAAAGTC CAGGTACTGC GGGAATCTCC GTTTTGAACA AGGCAAGCAG

1151 GCTGCCTGGA ACAGAACAAA GCGTCTCTGC CCTGGGGACA CAGGCCCACA

1201 CGGTCCAGAA CCCTGCACTG CTGCTGACAC CAGAAACTGA ACTAAAAGAG

1251 GAGAGTTTTA GTCCTCCGTG TTTCGTCCTA AAACACCTCT GTTTTGCACT

1301 GACCTGATGG GAAATAAATT ATATTAATTT TTAAACCCTT TCCGGTTGGA

1351 TGCCTAACAT TTAGGCAAGA GACAACAAAG AAAACCAGAG TCAACTCCCT

1401 TGAAATGTAG GAATAAAGGA TGCATAATAA ACAGGAAAGG CACAGGTTTT

1451 GAGAAGATCA GCCCACAGTG TTGTCCTTGA ATCAAACAAA ATGGTCGGAG

1501 GAACCCTTCG GGTTCAGCAC AAAGAGGTGA CTACAGCCTT TTGGTCACCA

1551 GATGACTCCG CCCCTTTGTA ATGAGTCTGC CAAGTAGACT CTATCAAGAT

1601 TCTGGGGAAA GGAGAAAGAA CACATTGACC TGCCCGGGCG GCCGCTCGAG

1651 CCCTATGA (SEQ ID NO:17)
```

FIG.6B

```
  1 MVGLQPSEVP PTTVVRFLGA GTAACFADLL TFPLDTAKVR LQIQGENPGA

 51 QSVQYRGVLG TILTMVRTEG PRSPYSGLVA GLHRQMSFAS IRIGLYDSVK

101 QFYTPKGADH SSVAIRILAG CTTGAMAVTC AQPTDVVKVR FQAMIRLGTG

151 GERKYRGTMD AYRTIAREEG VRGLWKGTWP NITRNAIVNC AEMVTYDIIK

201 EKLLESHLFT DNFPCHFVSA FGAGFCATVV ASPVDVVKTR YMNAPLGRYR

251 SPLHCMLKMV AQEGPTAFYK GFVPSFLRLG AWNVMMFVTY EQLRRALMKV

301 QVLRESPF* (SEQ ID NO:18)
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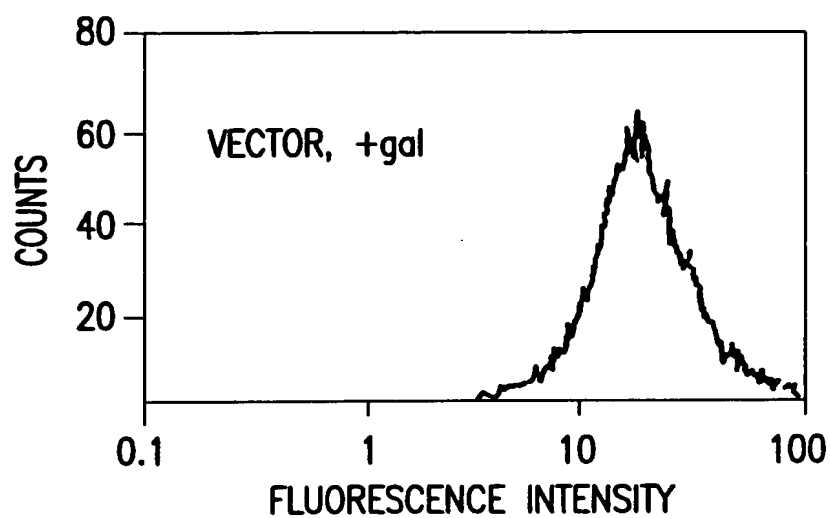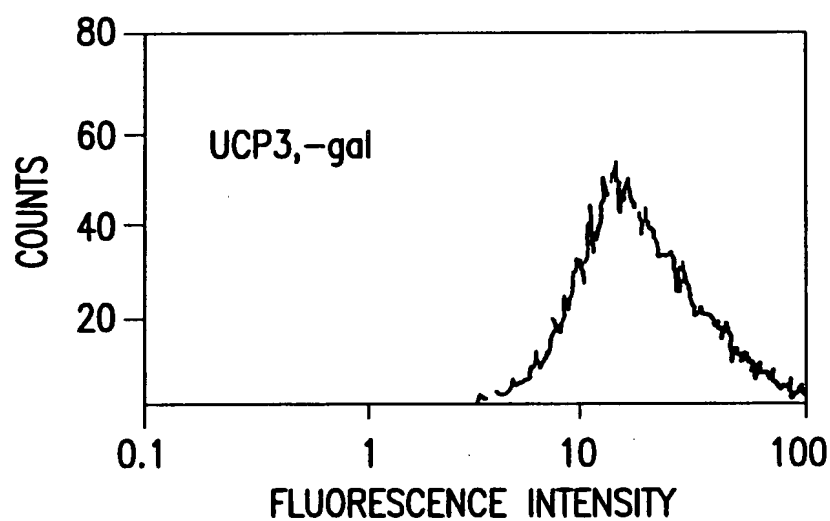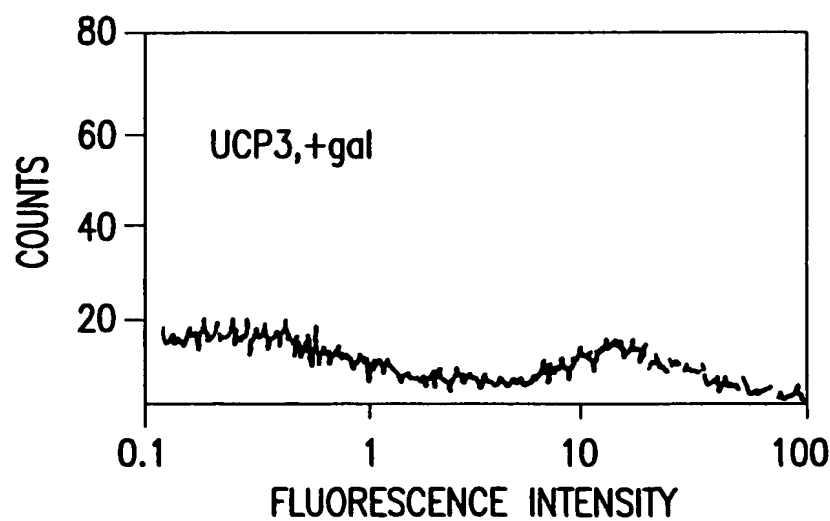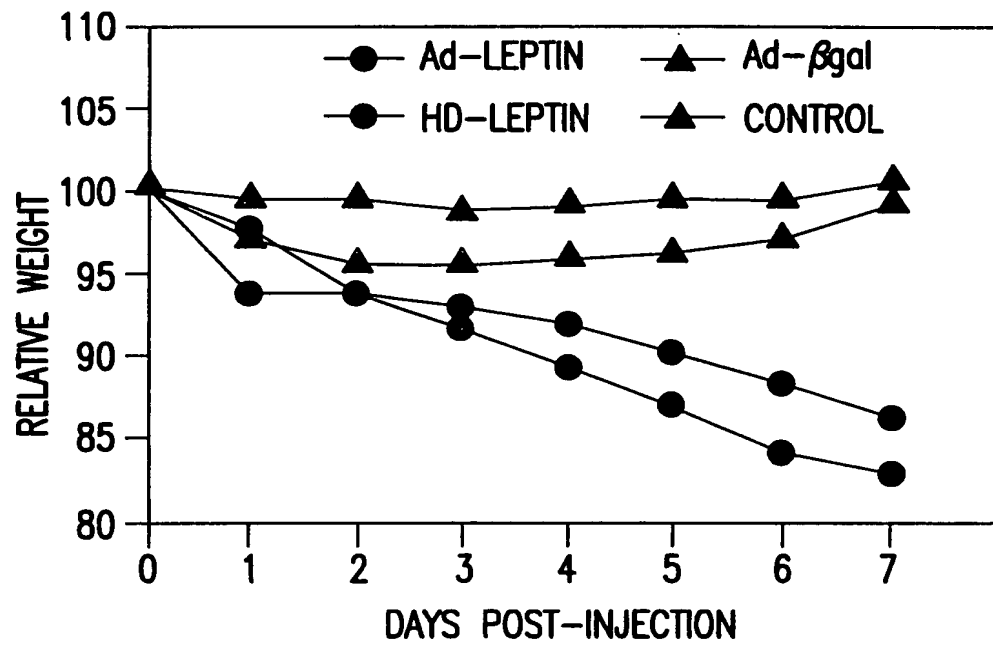
FIG.7

FIG.8A

VECTOR, +gal

COUNTS

80
60
40
20

0.1   1   10   100
FLUORESCENCE INTENSITY

FIG.8B

UCP3,-gal

COUNTS

80
60
40
20

0.1   1   10   100
FLUORESCENCE INTENSITY

FIG.8C

UCP3,+gal

COUNTS

80
60
40
20

0.1   1   10   100
FLUORESCENCE INTENSITY

FIG.9A

FIG.9B